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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq2-Peptides.res made by tport on Thu 10 Jul 103 11:28:49-PDT.


Query sequence being compared:US-09-508-832-2 (1-110)
Number of sequences searched:                  21
Number of scores above cutoff:                 21

      Results of the initial comparison of US-09-508-832-2 (1-110) with:
        File : US09508832.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-   **
Q     -     *
U     -       *                          *
E     -
N     -
C     -
E     - **      *                      **                          *
S    0----------------------------------------------------------------------
      |     ||      |      | |    |      |     ||      |     | |    |
SCORE 0     12     24     37 |   49     61     73     86     98 |  110
STDEV       0               1                 2                3


                          PARAMETERS

Similarity matrix       PAM-150     K-tuple                    1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty           20
Gap penalty               5.00     Window size              110
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                       SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                            25           11          29.71

Times:                    CPU                   Total Elapsed
                      00:00:00.00               00:00:00.00

Number of residues:                1041
Number of sequences searched:        21
Number of scores above cutoff:       21


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                          Init.  Opt.
Sequence Name    Description                     Length  Score  Score  Sig.  Frame
----------------------------------------------------------------------------------
  1. US-09-508-832-2 Sequence 2, Application US    110    110    110   2.86    0

The list of other best scores is:

                                                          Init.  Opt.
Sequence Name    Description                     Length  Score  Score  Sig.  Frame
----------------------------------------------------------------------------------
                    **** 1 standard deviation above mean ****
  2. US-09-508-832-4 Sequence 4, Application US    140     69    105   1.48    0
  3. US-09-508-832-6 Sequence 6, Application US    196     69     86   1.48    0
  4. US-09-508-832-8 Sequence 8, Application US    138     63     94   1.28    0
  5. US-09-508-832-10 Sequence 10, Application     198     61     69   1.21    0


1. US-09-508-832-2 (1-110)
   US-09-508-832-2 Sequence 2, Application US/09508832

Initial Score    =    110  Optimized Score  =    110  Significance =  2.86
Residue Identity =   100%  Matches         =    110  Mismatches   =     0
Gaps             =     0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQASIRQSQEEPEDLRPEIRIAQELRRIGDEFN
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQASIRQSQEEPEDLRPEIRIAQELRRIGDEFN
    X       10        20        30        40        50        60        70

          80        90       100        X
    ETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||
    ETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          80        90       100       110


2. US-09-508-832-2 (1-110)
   US-09-508-832-4 Sequence 4, Application US/09508832

Initial Score    =     69  Optimized Score  =    105  Significance =  1.48
Residue Identity =    78%  Matches         =    110  Mismatches   =     0
Gaps             =     30  Conservative Substitutions               =     0

    X       10        20        30        40
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQ------------------------------A
    ||||||||||||||||||||||||||||||||||||||||                               |
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    X       10        20        30        40        50        60        70

          50        60        70        80        90       100        X
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          80        90       100       110       120       130       140


3. US-09-508-832-2 (1-110)
   US-09-508-832-6 Sequence 6, Application US/09508832

Initial Score    =     69  Optimized Score  =     86  Significance =  1.48
Residue Identity =    45%  Matches         =     75  Mismatches   =    33
Gaps             =     54  Conservative Substitutions               =     2

                                  X       10        20        30
                                  MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQT--
                                                :     | ||     :     | | |
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
            10        20        30  X     40        50        60        70

                                                       40        50
    ---------------------------------------------------EPQASIRQSQEEPEDLRPEI
                                                       ||||||||||||||||||||
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
          80        90       100       110       120       130       140
```

```
    60        70        80        90       100       110
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
       150       160       170       180       190     X
```

4. US-09-508-832-2 (1-110)
   US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score	= 63	Optimized Score	= 94	Significance	= 1.28
Residue Identity	= 63%	Matches	= 87	Mismatches	= 21
Gaps	= 28	Conservative Substitutions		=	2

```
    X       10        20        30        40
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQASIRQS------------------------
    |||||||||||||||| |||||||||||||||||||||||||
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    X       10        20        30        40        50        60        70

        50        60        70        80        90       100       110
    ---QEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
       | || |:|||| |||||||||||||  | |||| | |  ||||| |||| |||:| ||||| |
    SMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
          80        90       100       110       120       130       X
```

5. US-09-508-832-2 (1-110)
   US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score	= 61	Optimized Score	= 69	Significance	= 1.21
Residue Identity	= 35%	Matches	= 48	Mismatches	= 58
Gaps	= 26	Conservative Substitutions		=	4

```
    X       10        20        30        40        50        60
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQASIRQSQEEPEDLRPEIRIAQEL--------
    |||||||||||||||| |||||||||||||||||||||:          |  |        |
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQGNPEGNHGGEGDSCPHGSPQGPLAPPASPGP
    X       10        20        30        40        50        60        70

                      70        80        90       100       110
    ------------------RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
                      |     |     |         :   |         :   :   |
    FATRSPLFIFMRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRP
          80        90       100       110       120       130     X 140

    EIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRL
       150       160       170       180
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq4-Peptides.res made by tport on Thu 10 Jul 103 11:30:19-PDT.


Query sequence being compared:US-09-508-832-4 (1-140)
Number of sequences searched:                  21
Number of scores above cutoff:                 21

      Results of the initial comparison of US-09-508-832-4 (1-140) with:
        File : US09508832.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-  **
Q     -
U     -    *
E     -     *
N     -
C     -
E    -**     *                    *   *      *  *                  *
S    0----------------------------------------------------------------
      |    | |      |       | |    |      |     ||      |       |  |   |
SCORE 0    |16     31      47 |   62     78     93     109     124  | 140
STDEV      0                 1                 2                 3


                        PARAMETERS

Similarity matrix       PAM-150     K-tuple                      1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty             20
Gap penalty               5.00     Window size                110
Gap size penalty          0.05
Cutoff score                 2
Randomization group          0

                     SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                            30           11       39.47

Times:                     CPU                   Total Elapsed
                     00:00:00.00                 00:00:00.00

Number of residues:                  1041
Number of sequences searched:          21
Number of scores above cutoff:         21


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                          Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
  1. US-09-508-832-4 Sequence 4, Application US    140   140   140   2.79   0

The list of other best scores is:

                                                          Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  2. US-09-508-832-6 Sequence 6, Application US    196    99   118   1.75   0
  3. US-09-508-832-8 Sequence 8, Application US    138    92   126   1.57   0
  4. US-09-508-832-10 Sequence 10, Application     198    78    82   1.22   0
                  ****  0 standard deviation from mean ****
  5. US-09-508-832-2 Sequence 2, Application US    110    69   105   0.99   0


1. US-09-508-832-4 (1-140)
   US-09-508-832-4 Sequence 4, Application US/09508832

Initial Score    =    140  Optimized Score  =    140  Significance =  2.79
Residue Identity =   100%  Matches          =    140  Mismatches   =     0
Gaps             =      0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130         X
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          80        90       100       110       120       130       140


2. US-09-508-832-4 (1-140)
   US-09-508-832-6 Sequence 6, Application US/09508832

Initial Score    =     99  Optimized Score  =    118  Significance =  1.75
Residue Identity =    73%  Matches          =    103  Mismatches   =    35
Gaps             =      0  Conservative Substitutions               =     2

                                                    X       10        20
                                                    MAKQPSDVSSECDREGGQLQPA
                                                      :   |     |       |
    DVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATRSPLFIF
      10        20        30        40        50      X 60        70

          30        40        50        60        70        80        90
    ERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEIRIAQEL
     |    |   :          ||||||||||||||||||||||||||||||||||||||||||||||||||||
    VRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEIRIAQEL
    80        90        100       110       120       130       140       150

       100       110       120       130       140
    RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||
    RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          160       170       180       190     X


3. US-09-508-832-4 (1-140)
   US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score    =     92  Optimized Score  =    126  Significance =  1.57
Residue Identity =    85%  Matches          =    120  Mismatches   =    15
Gaps             =      2  Conservative Substitutions               =     3

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
```

```
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    | ||:  || |:|||| ||||||||||||  | |||| | |  ||||| |||| |||:| ||||| |
    SMRQA--EPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
           80        90       100       110       120       130       X
```

4. US-09-508-832-4 (1-140)
   US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score	= 78	Optimized Score	= 82	Significance	= 1.22
Residue Identity	= 32%	Matches	= 53	Mismatches	= 82
Gaps	= 23	Conservative Substitutions		= 5	

```
    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    |||||||||||||||| ||||||||||||||||||||||||    :    :       |       |
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQGNPEGNHGGEGDSCPHGSPQGPLAPPASPGP
    X       10        20        30        40        50        60        70

                                80        90       100       110       120
    SIRQSQ----------------------EEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHP
        |                       :         :  |        ||              |:  |
    FATRSPLFIFMRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRP
          80        90       100       110       120       130       140

          130       140
    QMVILQLLRFIFRLVWRRH
       | | || |
    EIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
       150       160  X    170       180       190
```

5. US-09-508-832-4 (1-140)
   US-09-508-832-2 Sequence 2, Application US/09508832

Initial Score	= 69	Optimized Score	= 105	Significance	= 0.99
Residue Identity	= 78%	Matches	= 110	Mismatches	= 0
Gaps	= 30	Conservative Substitutions		= 0	

```
    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    |||||||||||||||||||||||||||||||||||||||||||||                       |
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQ-----------------------------A
    X       10        20        30        40

          80        90       100       110       120       130         X
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          50        60        70        80        90       100       110
```

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O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq6-peptides.res made by tport on Thu 10 Jul 103 11:31:54-PDT.


Query sequence being compared:US-09-508-832-6 (1-196)
Number of sequences searched:                  21
Number of scores above cutoff:                 21

      Results of the initial comparison of US-09-508-832-6 (1-196) with:
        File : US09508832.pep

   100-
     -
N    -
U   50-
M    -
B    -
E    -
R    -
     -
O    -
F   10-
     -
S    - *
E   5-  *
Q    -
U    -
E    -*  *
N    -
C    -
E    -    *              * *       *   *                          *
S   0----------------------------------------------------------------------
     |  |   |      |    | |       |     |       |      | |    |      |
SCORE 0  |  22     44    |65     87    109     131    152 |  174    196
STDEV    0              1               2               3

                        PARAMETERS

Similarity matrix       PAM-150     K-tuple                    1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty           20
Gap penalty               5.00     Window size              110
Gap size penalty          0.05
Cutoff score                 3
Randomization group          0

                     SEARCH STATISTICS

Scores:                 Mean       Median     Standard Deviation
                          33           11       49.41

Times:                  CPU                   Total Elapsed
                    00:00:00.00               00:00:00.00

Number of residues:                1041
Number of sequences searched:        21
Number of scores above cutoff:       21


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                        Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
  1. US-09-508-832-6 Sequence 6, Application US    196   196   196   3.30   0

The list of other best scores is:

                                                        Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  2. US-09-508-832-10 Sequence 10, Application     198   112   177   1.60   0
  3. US-09-508-832-4 Sequence 4, Application US    140    98   117   1.32   0
                  ****  0 standard deviation from mean ****
  4. US-09-508-832-8 Sequence 8, Application US    138    75    79   0.85   0
  5. US-09-508-832-2 Sequence 2, Application US    110    69    85   0.73   0


1. US-09-508-832-6 (1-196)
   US-09-508-832-6 Sequence 6, Application US/09508832

Initial Score     =    196  Optimized Score  =    196  Significance =  3.30
Residue Identity  =   100%  Matches          =    196  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
          80        90       100       110       120       130       140

       150       160       170       180       190     X
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
       150       160       170       180       190     X


2. US-09-508-832-6 (1-196)
   US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score     =    112  Optimized Score  =    177  Significance =  1.60
Residue Identity  =    86%  Matches          =    173  Mismatches   =    17
Gaps              =      6  Conservative Substitutions               =     4

    X       10        20        30        40            50        60
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPD----GEGDRCPHGSPQGPLAPPASPGP
    |||||||||||||||| ||||||||||||||||||||||||||:    |||| ||||||||||||||||||
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQGNPEGNHGGEGDSCPHGSPQGPLAPPASPGP
    X       10        20        30        40        50        60        70

    70        80        90       100       110       120       130       140
    FATRSPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDL
    |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||:  || |:
    FATRSPLFIFMRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASMRQA--EPADM
          80        90       100       110       120       130       140

         150       160       170       180       190     X
    RPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    |||| ||||||||||||  | |||| | |  ||||| |||| |||:| ||||| |
    RPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
         150       160       170       180       190       X


3. US-09-508-832-6 (1-196)
   US-09-508-832-4 Sequence 4, Application US/09508832

Initial Score     =     98  Optimized Score  =    117  Significance =  1.32
Residue Identity  =    73%  Matches          =    103  Mismatches   =    35
```

```
Gaps            =      0  Conservative Substitutions              =      2

      10        20        30        40        50      X 60        70
    DVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATRSPLFIF
                                                      :      |          |
                                                     MAKQPSDVSSECDREGGQLQPA
                                                     X       10        20

    80        90       100       110       120       130       140       150
    VRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEIRIAQEL
     |   |   :          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEIRIAQEL
          30        40        50        60        70        80        90

         160       170       180       190     X
    RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||
    RRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
       100       110       120       130       140


4. US-09-508-832-6 (1-196)
   US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score    =     75  Optimized Score  =     79  Significance =  0.85
Residue Identity =     33%  Matches          =     48  Mismatches   =    85
Gaps             =      5  Conservative Substitutions              =     5

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
    ||||||||||||||| ||||||||||||||||||||||||    :      |         |         |
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPA-----PMSCDKSTQTPSPPCQAFNHY
    X       10        20        30        40               50        60

          80        90       100       110       120       130       140  X
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
           | :           : :  |         :          ||                    |
    LSAMASMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
     70        80        90       100       110       120       130       X

       150       160       170       180       190
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVW


5. US-09-508-832-6 (1-196)
   US-09-508-832-2 Sequence 2, Application US/09508832

Initial Score    =     69  Optimized Score  =     85  Significance =  0.73
Residue Identity =     45%  Matches          =     75  Mismatches   =    33
Gaps             =     54  Conservative Substitutions              =     2

          10        20        30  X     40        50        60        70
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
                                      :     | ||     :     | | |
                                    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQT--
                                    X       10        20        30

          80        90       100       110       120       130       140
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
                                                              ||||||||||||||||
    ----------------------------------------------------------EPQASIRQSQEEPEDLRPEI
                                                             40        50

       150       160       170       180       190     X
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
    60        70        80        90       100       110
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq8-Peptides.res made by tport on Thu 10 Jul 103 11:32:57-PDT.


Query sequence being compared:US-09-508-832-8 (1-138)
Number of sequences searched:                  21
Number of scores above cutoff:                 21

      Results of the initial comparison of US-09-508-832-8 (1-138) with:
        File : US09508832.pep

   100-
      -
N     -
U  50-
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -
E   5-   **
Q     -
U     -
E     -  *
N     -
C     -
E    ***     **                 *    *       * *                  *
S   0----------------------------------------------------------------------
      |    | |      |       | |    |       |     ||       |       | |    |
SCORE 0    |15     31      46 |   61      77     92     107     123 |  138
STDEV      0                 1                  2                  3


                          PARAMETERS

Similarity matrix       PAM-150     K-tuple                      1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty             20
Gap penalty                5.00     Window size                110
Gap size penalty           0.05
Cutoff score                  2
Randomization group           0

                       SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             29           11          38.70

Times:                      CPU                    Total Elapsed
                      00:00:00.00                  00:00:00.00

Number of residues:                  1041
Number of sequences searched:          21
Number of scores above cutoff:         21


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                                 Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
  1. US-09-508-832-8 Sequence 8, Application US    138   138   138   2.82   0

The list of other best scores is:

                                                                 Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                  **** 1 standard deviation above mean ****
  2. US-09-508-832-10 Sequence 10, Application     198    97   116   1.76   0
  3. US-09-508-832-4 Sequence 4, Application US    140    92   126   1.63   0
  4. US-09-508-832-6 Sequence 6, Application US    196    75    80   1.19   0
                  **** 0 standard deviation from mean ****
  5. US-09-508-832-2 Sequence 2, Application US    110    63    94   0.88   0


1. US-09-508-832-8 (1-138)
   US-09-508-832-8 Sequence 8, Application US/09508832

Initial Score    =    138  Optimized Score  =    138  Significance =  2.82
Residue Identity =   100%  Matches          =    138  Mismatches   =     0
Gaps             =     0  Conservative Substitutions                =     0

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       X
    SMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
          80        90       100       110       120       130       X


2. US-09-508-832-8 (1-138)
   US-09-508-832-10 Sequence 10, Application US/09508832

Initial Score    =     97  Optimized Score  =    116  Significance =  1.76
Residue Identity =    73%  Matches          =    101  Mismatches   =    35
Gaps             =     0  Conservative Substitutions                =     2

                                                      X       10        20
                                                      MAKQPSDVSSECDREGRQLQPA
                                                                :       |
    ECDREGRQLQPAERPPQLRPGAPTSLQTEPQGNPEGNHGGEGDSCPHGSPQGPLAPPASPGPFATRSPLFIF
            20        30        40        50        60        70        80

          30        40        50        60        70        80        90
    ERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRPEIWIAQELRR
     |    |    :           ||||||||||||||||||||||||||||||||||||||||||||||||||||
    MRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRPEIWIAQELRR
          90        100       110       120       130       140       150

       100       110       120       130       X
    IGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
    ||||||||||||||||||||||||||||||||||||||||||||
    IGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
       160       170       180       190       X


3. US-09-508-832-8 (1-138)
   US-09-508-832-4 Sequence 4, Application US/09508832

Initial Score    =     92  Optimized Score  =    126  Significance =  1.63
Residue Identity =    85%  Matches          =    120  Mismatches   =    15
Gaps             =     2  Conservative Substitutions                =     3

    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
```

```
    X       10        20        30        40        50        60        70

            80        90       100       110       120       130       X
    SMRQA--EPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
    | ||:  || |:|||| ||||||||||||  | |||| | |  ||||| |||| |||:| ||||| |
    SIRQSQEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
          80        90       100       110       120       130       140
```

4. US-09-508-832-8 (1-138)
   US-09-508-832-6 Sequence 6, Application US/09508832

Initial Score	=	75	Optimized Score	=	80	Significance =	1.19
Residue Identity	=	33%	Matches	=	48	Mismatches =	85
Gaps	=	5	Conservative Substitutions			=	5

```
    X       10        20        30        40             50        60
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPA-----PMSCDKSTQTPSPPCQAFNHY
    |||||||||||||||| |||||||||||||||||||||||||    :     |         |      |
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQGNPDGEGDRCPHGSPQGPLAPPASPGPFATR
    X       10        20        30        40        50        60        70

     70        80        90       100       110       120       130       X
    LSAMASMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
          | :           : :  |         :        ||                  |
    SPLFIFVRRSSLLSRSSSGYFSFDTDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMASIRQSQEEPEDLRPEI
          80        90       100       110       120       130       140  X

    RIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVW
       150       160       170       180       190
```

5. US-09-508-832-8 (1-138)
   US-09-508-832-2 Sequence 2, Application US/09508832

Initial Score	=	63	Optimized Score	=	94	Significance =	0.88
Residue Identity	=	63%	Matches	=	87	Mismatches =	21
Gaps	=	28	Conservative Substitutions			=	2

```
    X       10        20        30        40        50        60        70
    MAKQPSDVSSECDREGRQLQPAERPPQLRPGAPTSLQTEPQDRSPAPMSCDKSTQTPSPPCQAFNHYLSAMA
    |||||||||||||||| ||||||||||||||||||||||||
    MAKQPSDVSSECDREGGQLQPAERPPQLRPGAPTSLQTEPQASIRQS------------------------
    X       10        20        30        40

          80        90       100       110       120       130       X
    SMRQAEPADMRPEIWIAQELRRIGDEFNAYYARRVFLNNYQAAEDHPRMVILRLLRYIVRLVWRMH
       | || |:|||| ||||||||||||  | |||| | |  ||||| |||| |||:| ||||| |
    ---QEEPEDLRPEIRIAQELRRIGDEFNETYTRRVFANDYREAEDHPQMVILQLLRFIFRLVWRRH
        50        60        70        80        90       100       110
```

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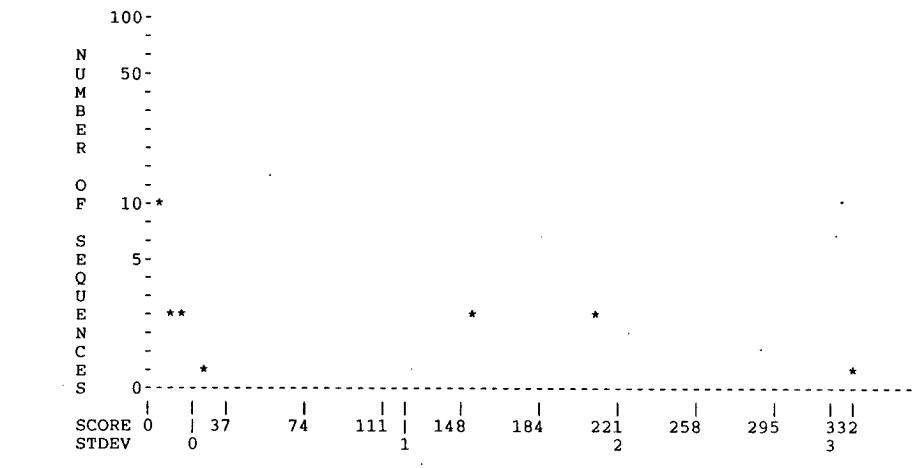
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq1-Nucs.res made by tport on Thu 10 Jul 103 11:35:13-PDT.


Query sequence being compared:US-09-508-832-1 (1-332)
Number of sequences searched:                  18
Number of scores above cutoff:                 18

      Results of the initial comparison of US-09-508-832-1 (1-332) with:
        File : US09508832.seq
```




```
                              PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              332
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean      Median      Standard Deviation
                             67          15                   98.37

Times:                      CPU                    Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                    2713
Number of sequences searched:            18
Number of scores above cutoff:           18


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                                  Init. Opt.
Sequence Name     Description                           Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
   1. US-09-508-832-1 Sequence 1, Application US    332   332   332   2.69   0

The list of other best scores is:

                                                                  Init. Opt.
Sequence Name     Description                           Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
                        ****  1 standard deviation above mean ****
   2. US-09-508-832-3 Sequence 3, Application US    422   209   298   1.44   0
   3. US-09-508-832-5 Sequence 5, Application US    590   209   245   1.44   0
                        ****  0 standard deviation from mean ****
   4. US-09-508-832-7 Sequence 7, Application US    416   151   240   0.85   0
   5. US-09-508-832-9 Sequence 9, Application US    596   151   193   0.85   0


1. US-09-508-832-1 (1-332)
   US-09-508-832-1 Sequence 1, Application US/09508832

Initial Score    =    332  Optimized Score  =    332  Significance =  2.69
Residue Identity =   100%  Matches          =    332  Mismatches   =     0
Gaps             =     0  Conservative Substitutions                =     0

    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGCTTCCATACGACAGTCTCAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGCTTCCATACGACAGTCTCAG
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    GAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAAC
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    GAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTA
     220       230       240       250       260       270       280

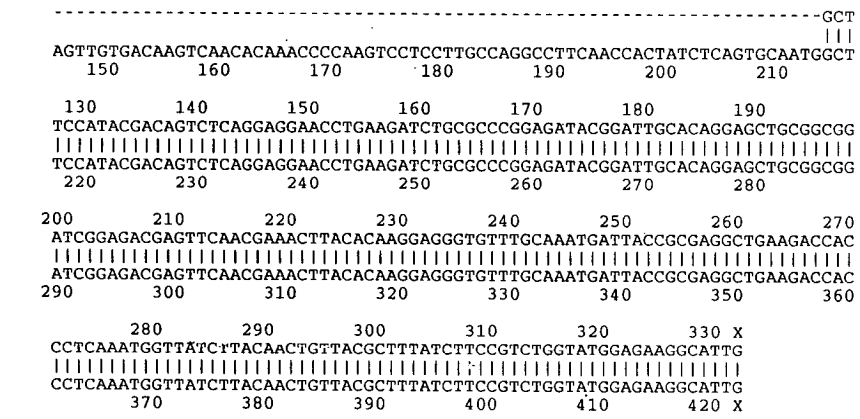
   290       300       310       320       330 X
    CAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
    |||||||||||||||||||||||||||||||||||||||||||
    CAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
   290       300       310       320       330 X


2. US-09-508-832-1 (1-332)
   US-09-508-832-3 Sequence 3, Application US/09508832

Initial Score    =    209  Optimized Score  =    298  Significance =  1.44
Residue Identity =    78%  Matches          =    332  Mismatches   =     0
Gaps             =     90  Conservative Substitutions                =     0

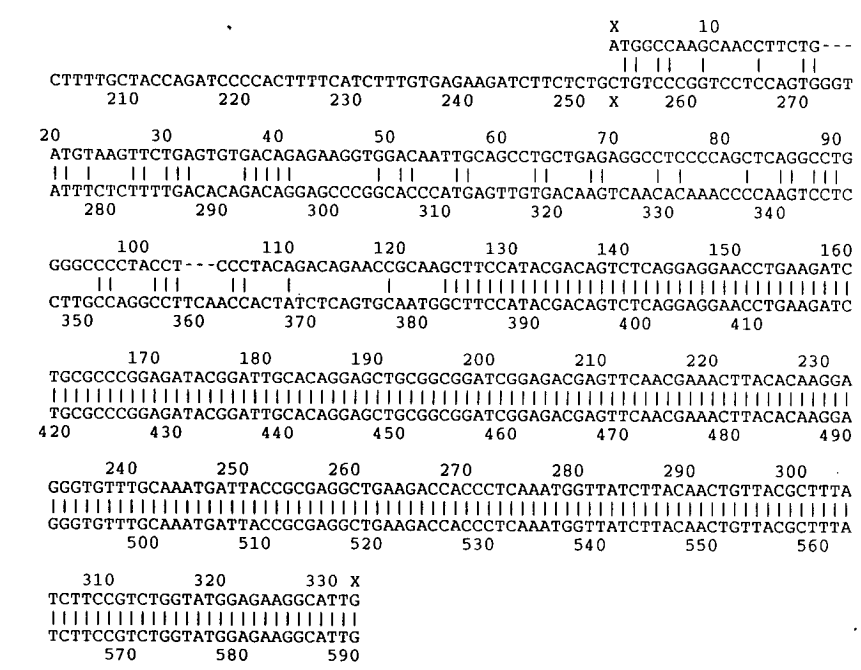
    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAA--------------------
    ||||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGACAGGAGCCCGGCACCCATG
          80        90       100       110       120       130       140
```



3. US-09-508-832-1 (1-332)
US-09-508-832-5 Sequence 5, Application US/09508832

Initial Score = 209 Optimized Score = 245 Significance = 1.44
Residue Identity = 75% Matches = 256 Mismatches = 76
Gaps = 6 Conservative Substitutions = 0



4. US-09-508-832-1 (1-332)
US-09-508-832-7 Sequence 7, Application US/09508832

Initial Score = 151 Optimized Score = 240 Significance = 0.85
Residue Identity = 65% Matches = 272 Mismatches = 60

Gaps = 84 Conservative Substitutions = 0

5. US-09-508-832-1 (1-332)
US-09-508-832-9 Sequence 9, Application US/09508832

Initial Score = 151 Optimized Score = 193 Significance = 0.85
Residue Identity = 62% Matches = 208 Mismatches = 124
Gaps = 3 Conservative Substitutions = 0

```
  TATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTG
500        510        520        530        540        550        560        570

  310        320        330 X
  TCCGTCTGGTATGGAGAAGGCATTG
  |||| ||||| ||||||| ||||||
  TCCGCCTGGTGTGGAGAATGCATTG
       580        590      X
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq3-nucs.res made by tport on Thu 10 Jul 103 11:38:26-PDT.


Query sequence being compared:US-09-508-832-3 (1-422)
Number of sequences searched:                  18
Number of scores above cutoff:                 18

      Results of the initial comparison of US-09-508-832-3 (1-422) with:
        File : US09508832.seq

   100-
      -
N     -
U  50-
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -*
E   5- *
Q     -
U     -
E     *
N     -
C     -
E     -   *                        *     *       *    *            *
S   0-----------------------------------------------------------------------
      |   |  |      |       |   |  |      |       |   |  |       |      |
SCORE 0   | 47     94     141   |188    234     281   |328    375    422
STDEV     0                     1                     2


                        PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              422
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             92           15      139.34

Times:                      CPU                   Total Elapsed
                    00:00:00.00                   00:00:00.00

Number of residues:                    2713
Number of sequences searched:            18
Number of scores above cutoff:           18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                                          Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   1. US-09-508-832-3 Sequence 3, Application US    422   422   422   2.37   0

The list of other best scores is:

                                                          Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
   2. US-09-508-832-7 Sequence 7, Application US    416   333   358   1.73   0
   3. US-09-508-832-5 Sequence 5, Application US    590   300   362   1.49   0
   4. US-09-508-832-9 Sequence 9, Application US    596   245   295   1.10   0
                    ****  0 standard deviation from mean ****
   5. US-09-508-832-1 Sequence 1, Application US    332   209   298   0.84   0


1. US-09-508-832-3 (1-422)
   US-09-508-832-3 Sequence 3, Application US/09508832

Initial Score     =    422  Optimized Score  =    422  Significance =  2.37
Residue Identity =   100%  Matches          =    422  Mismatches   =     0
Gaps              =     0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGACAGGAGCCCGGCACCCATG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGACAGGAGCCCGGCACCCATG
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    AGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGG
     220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    ATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCAC
   290       300       310       320       330       340       350       360

          370       380       390       400       410       420 X
    CCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
          370       380       390       400       410       420 X


2. US-09-508-832-3 (1-422)
   US-09-508-832-7 Sequence 7, Application US/09508832

Initial Score     =    333  Optimized Score  =    358  Significance =  1.73
Residue Identity =    86%  Matches          =    365  Mismatches   =    51
Gaps              =      6  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    ||||| |||||||||||||||||||||||||||||| |||||||| ||||||||||||||| ||||||
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
```
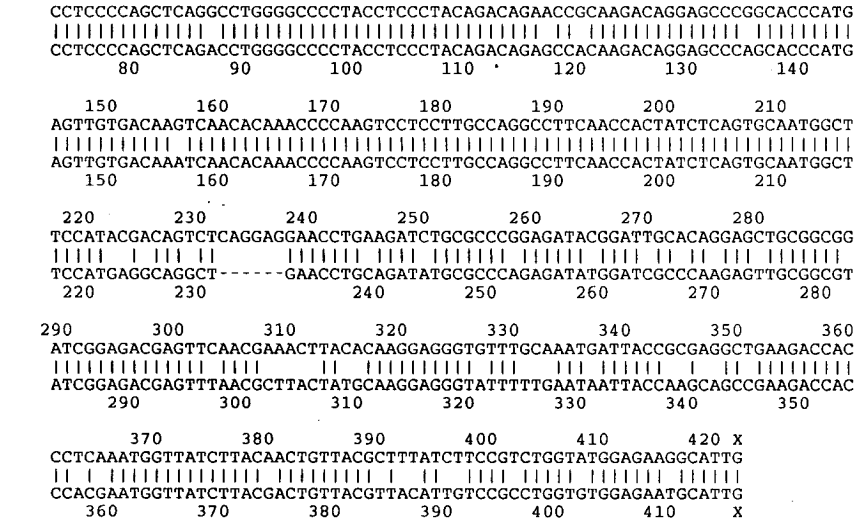
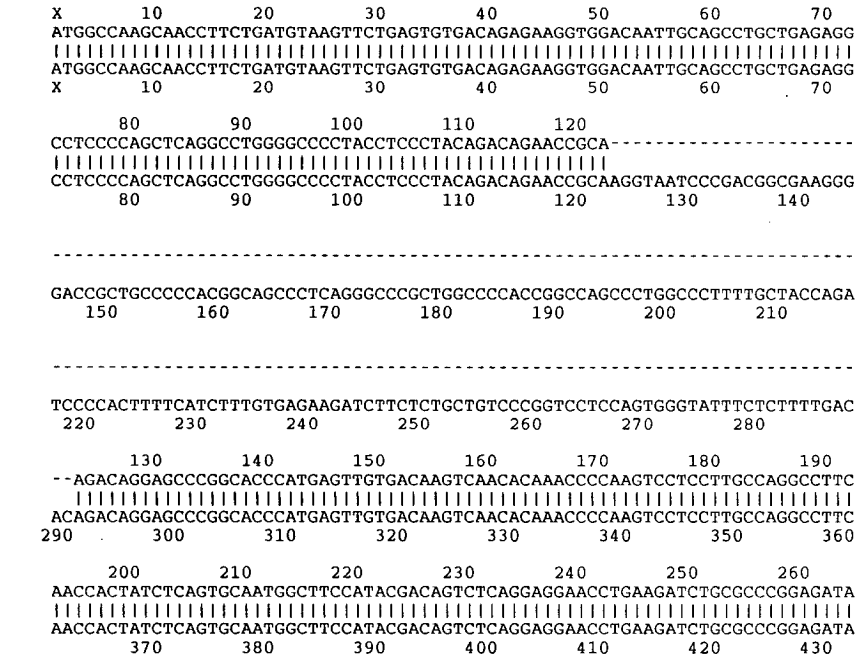
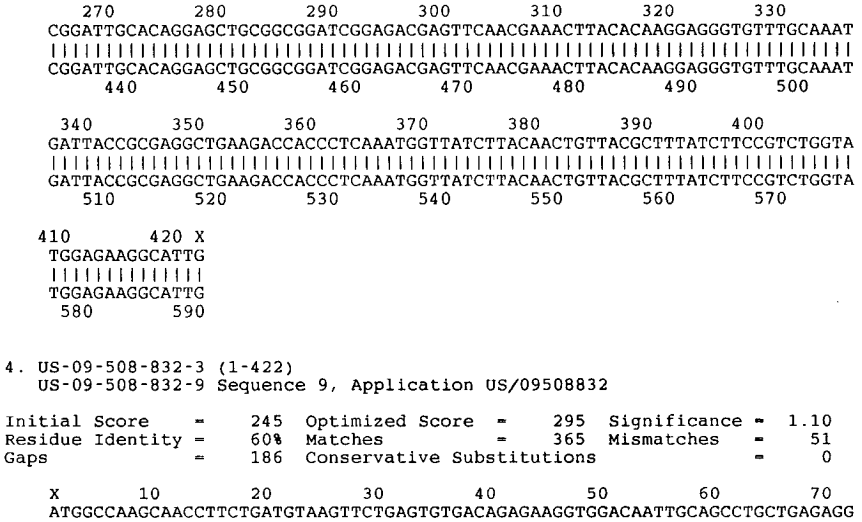



3. US-09-508-832-3 (1-422)
US-09-508-832-5 Sequence 5, Application US/09508832

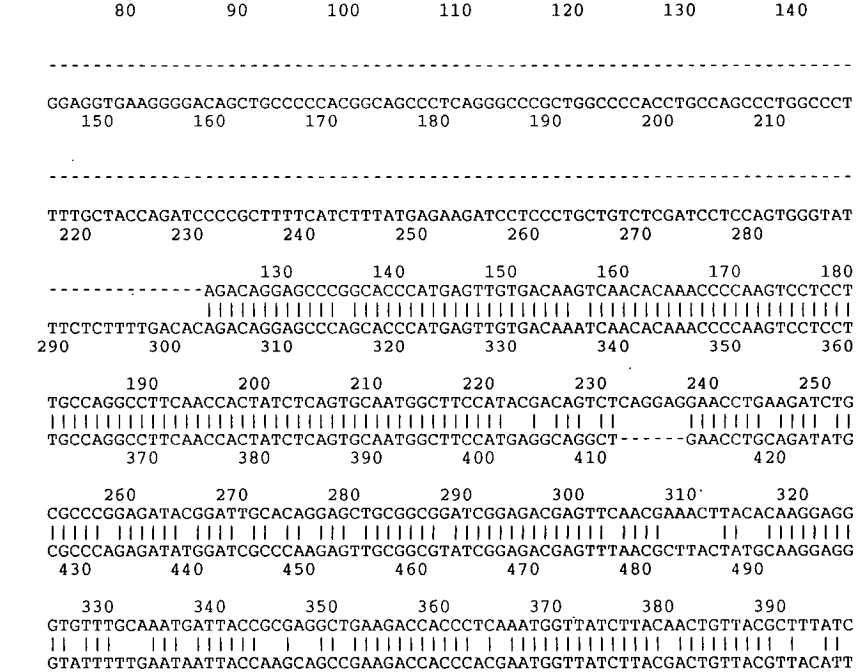
Initial Score	=	300	Optimized Score	=	362	Significance	= 1.49
Residue Identity	=	71%	Matches	=	422	Mismatches	= 0
Gaps	=	168	Conservative Substitutions				= 0





4. US-09-508-832-3 (1-422)
US-09-508-832-9 Sequence 9, Application US/09508832

Initial Score	=	245	Optimized Score	=	295	Significance	= 1.10
Residue Identity	=	60%	Matches	=	365	Mismatches	= 51
Gaps	=	186	Conservative Substitutions				= 0



```
 400       410       420 X
TTCCGTCTGGTATGGAGAAGGCATTG
 |||| ||||| ||||||| ||||||
GTCCGCCTGGTGTGGAGAATGCATTG
       580       590     X
```

5. US-09-508-832-3 (1-422)
US-09-508-832-1 Sequence 1, Application US/09508832

Initial Score	=	209	Optimized Score	=	298	Significance =	0.84
Residue Identity	=	78%	Matches	=	332	Mismatches =	0
Gaps	=	90	Conservative Substitutions			=	0

```
X       10        20        30        40        50        60        70
ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
X       10        20        30        40        50        60        70

      80        90       100       110       120       130       140
CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGACAGGAGCCCGGCACCCATG
|||||||||||||||||||||||||||||||||||||||||||||||||||
CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAA----------------------
      80        90       100       110       120

   150       160       170       180       190       200       210
AGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT
                                                                     |||
-------------------------------------------------------------------GCT


 220       230       240       250       260       270       280
TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGG
 130       140       150       160       170       180       190

290       300       310       320       330       340       350       360
ATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCAC
200       210       220       230       240       250       260       270

      370       380       390       400       410       420 X
CCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
      280       290       300       310       320       330 X
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq5-nucs.res made by tport on Thu 10 Jul 103 11:40:52-PDT.


Query sequence being compared:US-09-508-832-5 (1-590)
Number of sequences searched:                  18
Number of scores above cutoff:                 18

      Results of the initial comparison of US-09-508-832-5 (1-590) with:
        File : US09508832.seq
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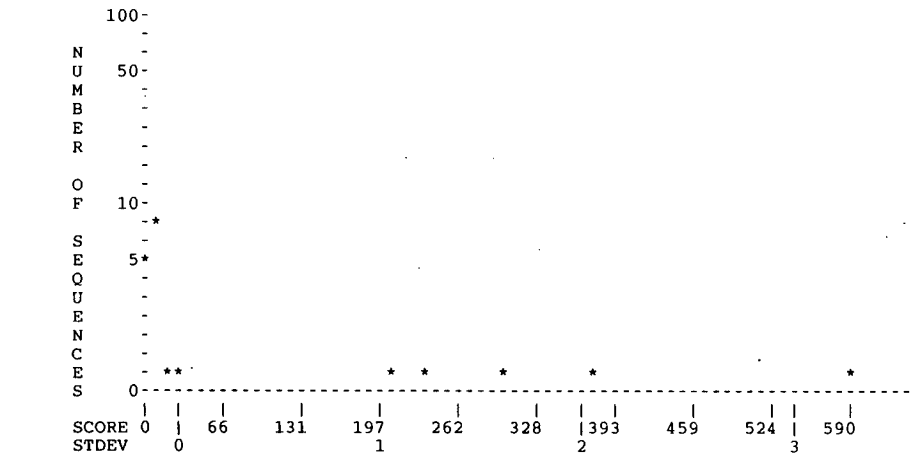

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	104	15	168.96

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	2713
Number of sequences searched:	18
Number of scores above cutoff:	18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-508-832-5	Sequence 5, Application US	590	590	590	2.88	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
2. US-09-508-832-9	Sequence 9, Application US	596	374	508	1.60	0
3. US-09-508-832-3	Sequence 3, Application US	422	300	362	1.16	0
	**** 0 standard deviation from mean ****					
4. US-09-508-832-7	Sequence 7, Application US	416	238	299	0.79	0
5. US-09-508-832-1	Sequence 1, Application US	332	209	245	0.62	0

1. US-09-508-832-5 (1-590)
   US-09-508-832-5 Sequence 5, Application US/09508832

Initial Score	= 590	Optimized Score	= 590	Significance	= 2.88
Residue Identity	= 100%	Matches	= 590	Mismatches	= 0
Gaps	= 0	Conservative Substitutions			= 0

```
X       10        20        30        40        50        60        70
ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
X       10        20        30        40        50        60        70

       80        90       100       110       120       130       140
CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGACGGCGAAGGG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGACGGCGAAGGG
       80        90       100       110       120       130       140

   150       160       170       180       190       200       210
GACCGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCGCCACCGGCCAGCCCTGGCCCTTTTGCTACCAGA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GACCGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCCCCACCGGCCAGCCCTGGCCCTTTTGCTACCAGA
   150       160       170       180       190       200       210

 220       230       240       250       260       270       280
TCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTGAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTGAC
 220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
ACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
290       300       310       320       330       340       350       360

       370       380       390       400       410       420       430
AACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATA
       370       380       390       400       410       420       430

     440       450       460       470       480       490       500
CGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAAT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAAT
     440       450       460       470       480       490       500

   510       520       530       540       550       560       570
GATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTA
   510       520       530       540       550       560       570

 580       X
TGGAGAAGGCATTG
|||||||||||||||
```

```
    TGGAGAAGGCATTG
     580       590
```

2. US-09-508-832-5 (1-590)
   US-09-508-832-9 Sequence 9, Application US/09508832

Initial Score	=	374	Optimized Score	=	508	Significance =	1.60
Residue Identity	=	86%	Matches	=	523	Mismatches =	61
Gaps	=	18	Conservative Substitutions			=	0

```
    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    |||||| |||||||||||||||||||||||||||||||||||| |||||||| |||||||||||||||| ||||||
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGACGGC------
    |||||||||||||| |||||||||||||||||||||||||||||||| || |||||||||||| || |||
    CCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAGGTAATCCTGAAGGCAATCAC
          80        90       100       110       120       130       140

         140       150       160       170       180       190       200
    ------GAAGGGGACCGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCCCCACCGGCCAGCCCTGGCCCT
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
    GGAGGTGAAGGGGACAGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCCCCACCTGCCAGCCCTGGCCCT
       150       160       170       180       190       200       210

       210       220       230       240       250       260       270
    TTTGCTACCAGATCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTAT
    |||||||||||||||| |||||||||||| |||||||||| || |||||||| || ||||||||||||||||
    TTTGCTACCAGATCCCCGCTTTTCATCTTTATGAGAAGATCCTCCCTGCTGTCTCGATCCTCCAGTGGGTAT
     220       230       240       250       260       270       280

     280       290       300       310       320       330       340
    TTCTCTTTTGACACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCT
    |||||||||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||
    TTCTCTTTTGACACAGACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCT
   290       300       310       320       330       340       350       360

   350       360       370       380       390       400       410       420
    TGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTG
    |||||||||||||||||||||||||||||||||||||||  | ||| ||      ||||||| |||| ||
    TGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTTCCATGAGGCAGGCT------GAACCTGCAGATATG
           370       380       390       400       410           420

           430       440       450       460       470       480       490
    CGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGG
    ||||| |||||| |||| || || ||| ||||||| |||||||||||||| ||||     ||  ||||||||
    CGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGAGACGAGTTTAACGCTTACTATGCAAGGAGG
     430       440       450       460       470       480       490

         500       510       520       530       540       550       560
    GTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATC
    || |||   ||| ||||||  |  || ||||||||||| | |||||||||||||| ||||||||| |  ||
    GTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATT
   500       510       520       530       540       550       560       570

      570       580       590
    TTCCGTCTGGTATGGAGAAGGCATTG
     |||| ||||| ||||||| ||||||
    GTCCGCCTGGTGTGGAGAATGCATTG
           580       590     X
```

3. US-09-508-832-5 (1-590)
   US-09-508-832-3 Sequence 3, Application US/09508832

Initial Score	=	300	Optimized Score	=	362	Significance =	1.16
Residue Identity	=	71%	Matches	=	422	Mismatches =	0
Gaps	=	168	Conservative Substitutions			=	0

```
    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCA----------------------
    |||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCA----------------------
          80        90       100       110       120

       150       160       170       180       190       200       210
    GACCGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCCCCACCGGCCAGCCCTGGCCCTTTTGCTACCAGA

    ------------------------------------------------------------------------


     220       230       240       250       260       270       280
    TCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTGAC

    ------------------------------------------------------------------------


   290       300       310       320       330       340       350       360
    ACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    --AGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
          130       140       150       160       170       180       190

          370       380       390       400       410       420       430
    AACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATA
         200       210       220       230       240       250       260

         440       450       460       470       480       490       500
    CGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAAT
       270       280       290       300       310       320       330

      510       520       530       540       550       560       570
    GATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTA
     340       350       360       370       380       390       400

     580       590
    TGGAGAAGGCATTG
    ||||||||||||||
    TGGAGAAGGCATTG
   410       420 X
```

4. US-09-508-832-5 (1-590)
   US-09-508-832-7 Sequence 7, Application US/09508832

Initial Score	=	238	Optimized Score	=	299	Significance =	0.79
Residue Identity	=	61%	Matches	=	365	Mismatches =	51
Gaps	=	174	Conservative Substitutions			=	0

```
    X       10        20        30        40        50        60        70
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    |||||| |||||||||||||||||||||||||||||| |||||||| |||||||||||||||| ||||||
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGGTAATCCCGACGGCGAAGGG
    |||||||||||||| |||||||||||||||||||||||||||||| || ||
    CCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACA----------------------
          80        90       100       110       120
```

```
   150       160       170       180       190       200       210
GACCGCTGCCCCCACGGCAGCCCTCAGGGCCCGCTGGCCCCACCGGCCAGCCCTGGCCCTTTTGCTACCAGA

 220       230       240       250       260       270       280
TCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGTATTTCTCTTTTGAC

290       300       310       320       330       340       350       360
ACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
--AGACAGGAGCCCAGCACCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTC
        130       140       150       160       170       180       190

        370       380       390       400       410       420       430
AACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATA
AACCACTATCTCAGTGCAATGGCTTCCATGAGGCAGGCT------GAACCTGCAGATATGCGCCCAGAGATA
      200       210       220       230               240       250

      440       450       460       470       480       490       500
CGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAAT
TGGATCGCCCAAGAGTTGCGGCGTATCGGAGACGAGTTTAACGCTTACTATGCAAGGAGGGTATTTTTGAAT
260       270       280       290       300       310       320       330

   510       520       530       540       550       560       570
GATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTA
AATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTG
        340       350       360       370       380       390       400

 580       590
TGGAGAAGGCATTG
TGGAGAATGCATTG
     410     X
```

5. US-09-508-832-5 (1-590)
   US-09-508-832-1 Sequence 1, Application US/09508832

Initial Score	=	209	Optimized Score	=	245	Significance =	0.62
Residue Identity	=	75%	Matches	=	256	Mismatches =	76
Gaps	=	6	Conservative Substitutions			=	0

```
      210       220       230       240       250  X    260       270
CTTTTGCTACCAGATCCCCACTTTTCATCTTTGTGAGAAGATCTTCTCTGCTGTCCCGGTCCTCCAGTGGGT
                                                  ATGGCCAAGCAACCTTCTG---
                                                  X       10

   280       290       300       310       320       330       340
ATTTCTCTTTTGACACAGACAGGAGCCCGGCACCCATGAGTTGTGACAAGTCAACACAAACCCCAAGTCCTC
ATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGGCCTCCCCAGCTCAGGCCTG
20        30        40        50        60        70        80        90

  350       360       370       380       390       400       410
CTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATC
GGGCCCCTACCT---CCCTACAGACAGAACCGCAAGCTTCCATACGACAGTCTCAGGAGGAACCTGAAGATC
      100       110       120       130       140       150       160

420       430       440       450       460       470       480       490
TGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGA
TGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGAGACGAGTTCAACGAAACTTACACAAGGA
```

```
      170       180       190       200       210       220       230

      500       510       520       530       540       550       560
GGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTA
GGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAAATGGTTATCTTACAACTGTTACGCTTTA
    240       250       260       270       280       290       300

    570       580       590
TCTTCCGTCTGGTATGGAGAAGGCATTG
TCTTCCGTCTGGTATGGAGAAGGCATTG
  310       320       330 X
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq7-nucs.res made by tport on Thu 10 Jul 103 11:43:17-PDT.


Query sequence being compared:US-09-508-832-7 (1-416)
Number of sequences searched:                  18
Number of scores above cutoff:                 18

      Results of the initial comparison of US-09-508-832-7 (1-416) with:
        File : US09508832.seq
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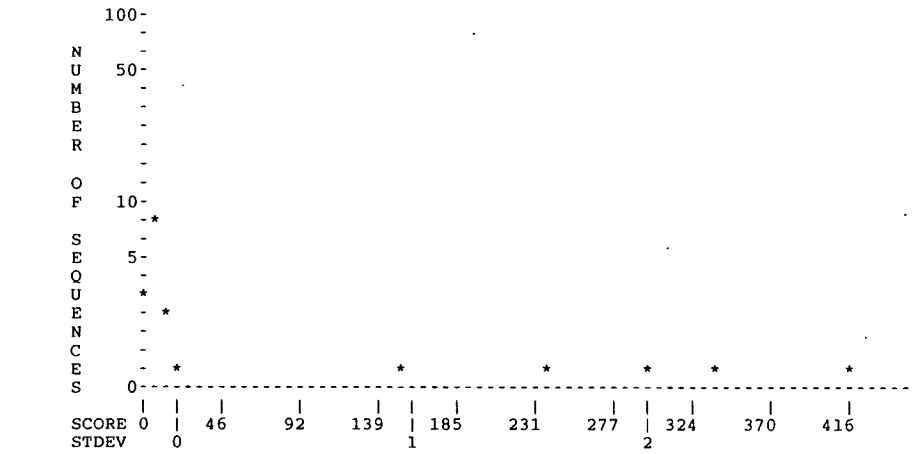


PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	416
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	87	13	135.78

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	2713
Number of sequences searched:	18
Number of scores above cutoff:	18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-508-832-7	Sequence 7, Application US	416	416	416	2.42	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
2. US-09-508-832-3	Sequence 3, Application US	422	333	358	1.81	0
3. US-09-508-832-9	Sequence 9, Application US	596	294	352	1.52	0
4. US-09-508-832-5	Sequence 5, Application US	590	238	299	1.11	0
	**** 0 standard deviation from mean ****					
5. US-09-508-832-1	Sequence 1, Application US	332	151	240	0.47	0

1. US-09-508-832-7 (1-416)
   US-09-508-832-7 Sequence 7, Application US/09508832

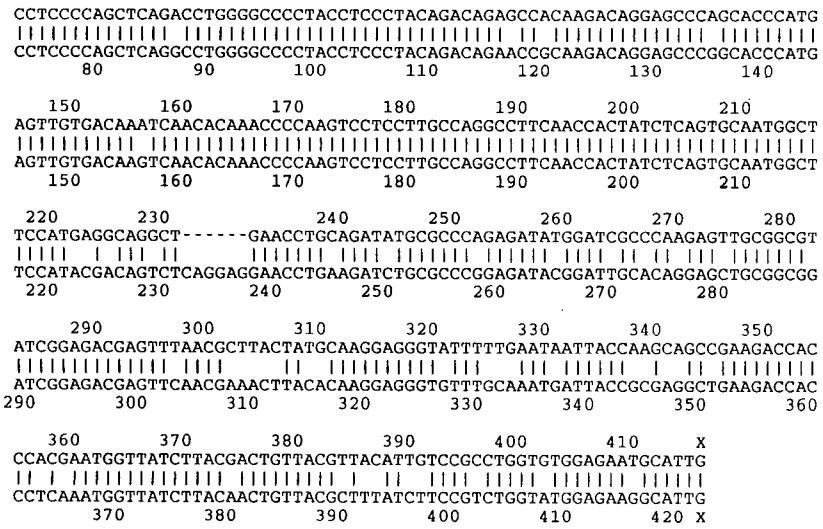
Initial Score	= 416	Optimized Score	= 416	Significance =	2.42
Residue Identity	= 100%	Matches	= 416	Mismatches =	0
Gaps	= 0	Conservative Substitutions		=	0

```
    X       10        20        30        40        50        60        70
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    X       10        20        30        40        50        60        70

           80        90       100       110       120       130       140
    CCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAGACAGGAGCCCAGCACCCATG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAGACAGGAGCCCAGCACCCATG
           80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    AGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGA
     220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
    GACGAGTTTAACGCTTACTATGCAAGGAGGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GACGAGTTTAACGCTTACTATGCAAGGAGGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGA
290       300       310       320       330       340       350       360

           370       380       390       400       410     X
    ATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTG
           370       380       390       400       410     X
```

2. US-09-508-832-7 (1-416)
   US-09-508-832-3 Sequence 3, Application US/09508832

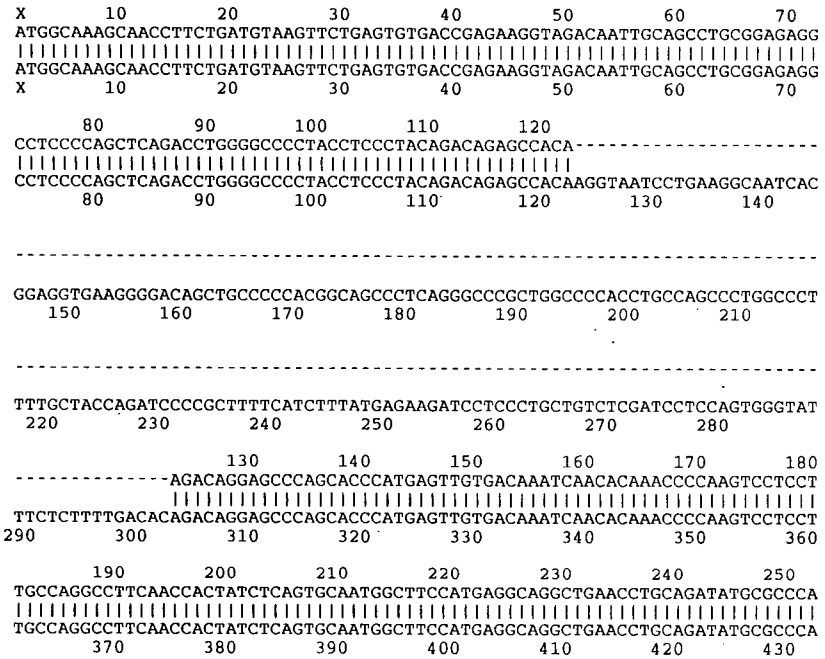
Initial Score	= 333	Optimized Score	= 358	Significance =	1.81
Residue Identity	= 86%	Matches	= 365	Mismatches =	51
Gaps	= 6	Conservative Substitutions		=	0

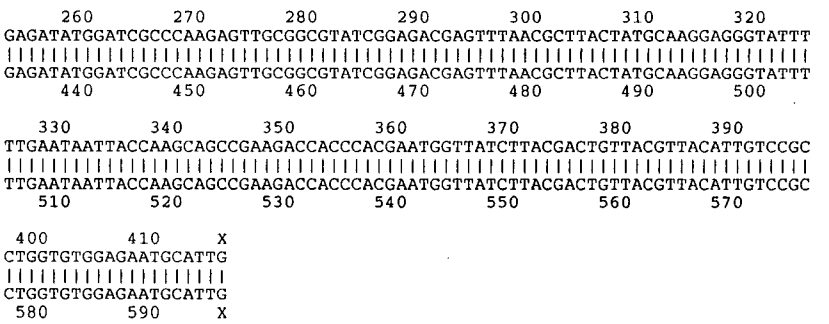
```
    X       10        20        30        40        50        60        70
    ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
    ||||| |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||| ||||||
    ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
    X       10        20        30        40        50        60        70

           80        90       100       110       120       130       140
```



3. US-09-508-832-7 (1-416)
US-09-508-832-9 Sequence 9, Application US/09508832

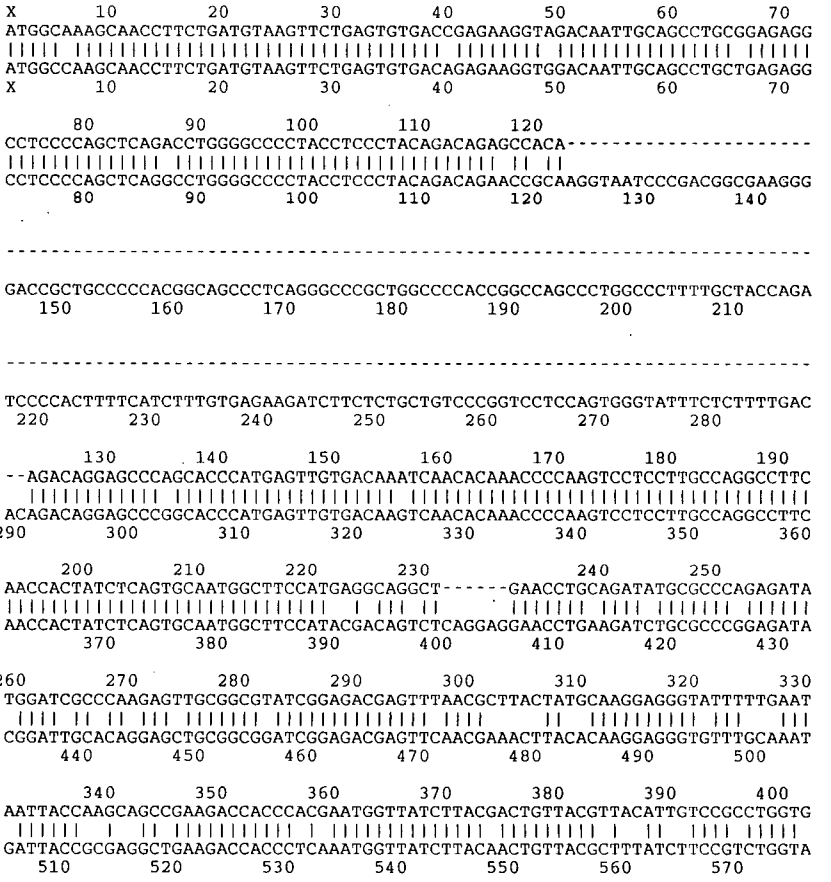
Initial Score = 294 Optimized Score = 352 Significance = 1.52
Residue Identity = 69% Matches = 416 Mismatches = 0
Gaps = 180 Conservative Substitutions = 0





4. US-09-508-832-7 (1-416)
US-09-508-832-5 Sequence 5, Application US/09508832

Initial Score = 238 Optimized Score = 299 Significance = 1.11
Residue Identity = 61% Matches = 365 Mismatches = 51
Gaps = 174 Conservative Substitutions = 0



```
     410     X
TGGAGAATGCATTG
||||||| ||||||
TGGAGAAGGCATTG
 580       590
```

5. US-09-508-832-7 (1-416)
US-09-508-832-1 Sequence 1, Application US/09508832

Initial Score	=	151	Optimized Score	=	240	Significance	= 0.47
Residue Identity	=	65%	Matches	=	272	Mismatches	= 60
Gaps	=	84	Conservative Substitutions			=	0

```
X       10        20        30        40        50        60        70
ATGGCAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAAGGTAGACAATTGCAGCCTGCGGAGAGG
|||||  |||||||||||||||||||||||||||||||||| ||||||||  ||||||||||||||| ||||||
ATGGCCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACAGAGAAGGTGGACAATTGCAGCCTGCTGAGAGG
X       10        20        30        40        50        60        70

      80        90       100       110       120       130       140
CCTCCCCAGCTCAGACCTGGGGCCCCTACCTCCCTACAGACAGAGCCACAAGACAGGAGCCCAGCACCCATG
|||||||||||||| ||||||||||||||||||||||||||||| || ||||     |  | |
CCTCCCCAGCTCAGGCCTGGGGCCCCTACCTCCCTACAGACAGAACCGCAAGCTTCCATACGA---------
      80        90       100       110       120       130

   150       160       170       180       190       200       210
AGTTGTGACAAATCAACACAAACCCCAAGTCCTCCTTGCCAGGCCTTCAACCACTATCTCAGTGCAATGGCT

---------------------------------------------------------------------------


 220       230       240       250       260       270       280
TCCATGAGGCAGGCTGAACCTGCAGATATGCGCCCAGAGATATGGATCGCCCAAGAGTTGCGGCGTATCGGA
     |   ||||  ||||||| |||| ||||||| |||||| |||| || || ||| ||||||| ||||||
---CAGTCTCAGGAGGAACCTGAAGATCTGCGCCCGGAGATACGGATTGCACAGGAGCTGCGGCGGATCGGA
    140       150       160       170       180       190       200

290       300       310       320       330       340       350       360
GACGAGTTTAACGCTTACTATGCAAGGAGGGTATTTTTGAATAATTACCAAGCAGCCGAAGACCACCCACGA
||||||||  ||||     ||  |||||||||| |||   ||| ||||||  |  || ||||||||||| | |
GACGAGTTCAACGAAACTTACACAAGGAGGGTGTTTGCAAATGATTACCGCGAGGCTGAAGACCACCCTCAA
   210       220       230       240       250       260       270

       370       380       390       400       410     X
ATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTGGTGTGGAGAATGCATTG
|||||||||||||  |||||||||  |   ||  |||| |||||  |||||||  ||||||
ATGGTTATCTTACAACTGTTACGCTTTATCTTCCGTCTGGTATGGAGAAGGCATTG
 280       290       300       310       320       330 X
```